

Power Simulation

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R Study Simulation

```
install.packages("simstudy")
install.packages("sjstats")
install.packages("tidyverse")

library(simstudy)
library(sjstats)
library(tidyverse)
```

Define Values

```
n <- 150      # sample size per group
group1 <- 2.00 # true mean treatment 1
group2 <- 2.10 # true mean treatment 2
group3 <- 2.20 # true mean treatment 3

sigma <- 0.40 # true SD for all groups
reps <- 10000 # number of simulations
```

p-value approach:

```
pvalues_pw_bh <- numeric(reps)

set.seed(1)
```

create progress bar

```
widthnew <- getOption("width")-23
pb <- txtProgressBar(min = 0, max = reps, style = 3, width = widthnew)
```

Run Loop

Idea: <https://goo.gl/dEr7dh>

```
for (i in 1:reps) {
  def <- defData(varname = "paffected",
                 dist = "normal", formula = group1,
                 variance = sigma, id = "idnum")
```

```

dtstudy1 <- genData(n, def)

def <- defData(varname = "paffected",
              dist = "normal", formula = group2,
              variance = sigma, id = "idnum")
dtstudy2 <- genData(n, def)

def <- defData(varname = "paffected",
              dist = "normal", formula = group3,
              variance = sigma, id = "idnum")
dtstudy3 <- genData(n, def)

dtstudy1 <- dtstudy1 %>% mutate(treatment = 1)
dtstudy2 <- dtstudy2 %>% mutate(treatment = 2)
dtstudy3 <- dtstudy3 %>% mutate(treatment = 3)

study <- bind_rows(dtstudy1, dtstudy2, dtstudy3)

study$treatment_factor <- factor(study$treatment)

posthoc_pw_bh <- pairwise.t.test(study$paffected, study$treatment_factor,
                               p.adjust.method = "BH")
posthoc_pw_bh <- pairwise.t.test(study$paffected, study$treatment_factor,
                               p.adjust.method = "BH")

#pvalues_pw_bh[i] <- posthoc_pw_bh[["p.value"]][1,1]      #1vs2
pvalues_pw_bh[i+reps] <- posthoc_pw_bh[["p.value"]][2,1]  #1vs3
#pvalues_pw_bh[i+reps*5] <- posthoc_pw_bh[["p.value"]][2,2] #2vs3

```

update progress bar

```
setTxtProgressBar(pb, i) }
```

End progress bar

```
close(pb)
```

Power

```
mean(pvalues_pw_bh < 0.05, na.rm = TRUE)
0.8244
```